

FIG 1

Reconstitution of lysis with anti KIR2D mAb on C1R  
Cw4 target at effector /target ratio of 4/1

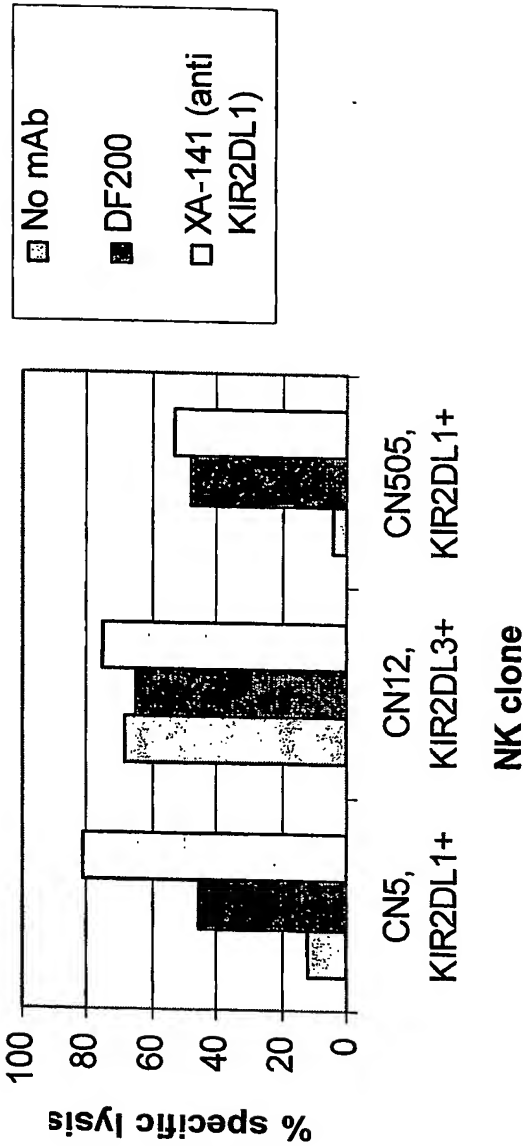


FIG 2

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FIG 3

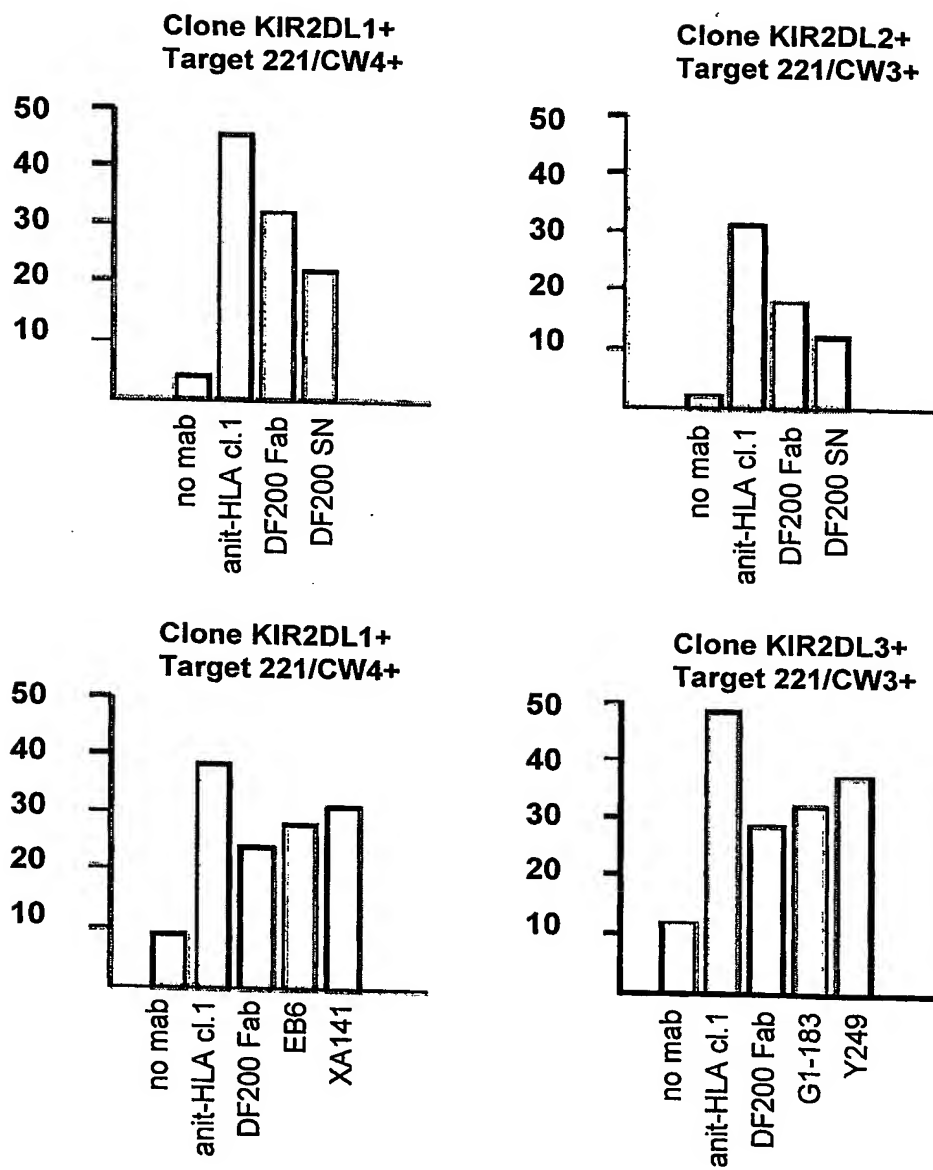
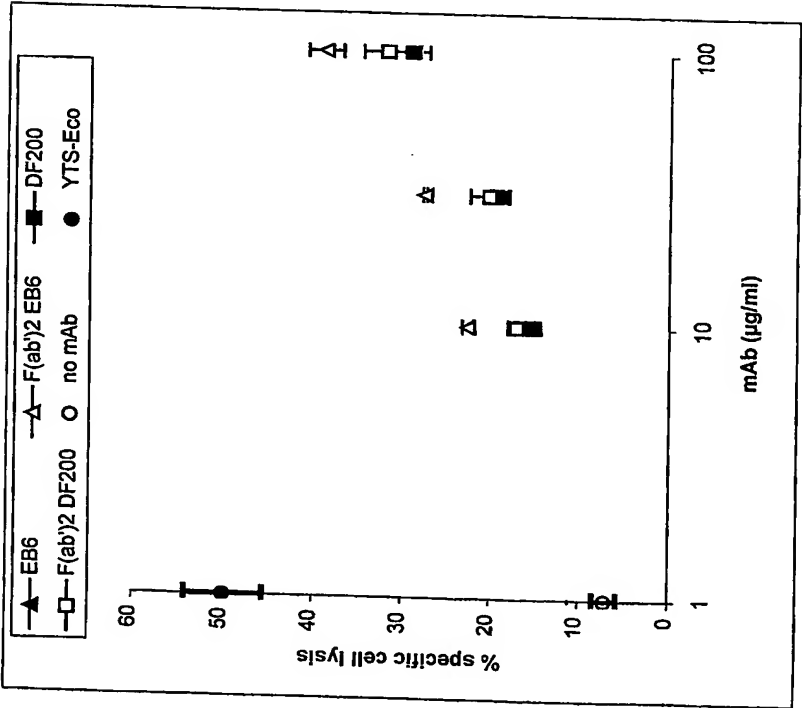


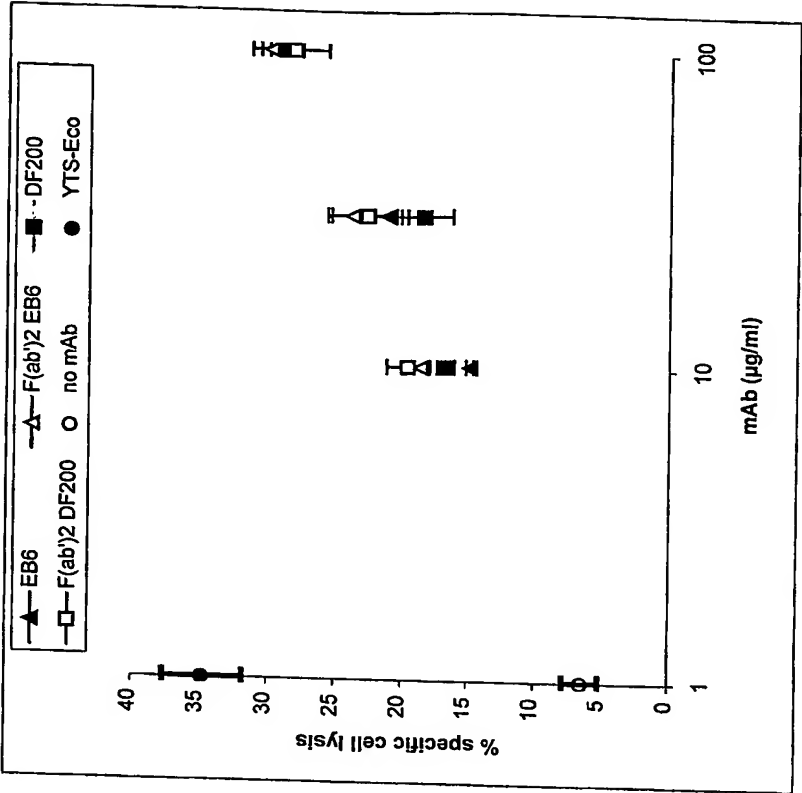
FIG 4

Target cell: FIG 4A : 721.221-cw4



E/T ratio= 1

FIG 4B : TUBO



E/T ratio= 2

FIG 5

FIG 5B : mAb: 10µg/ml

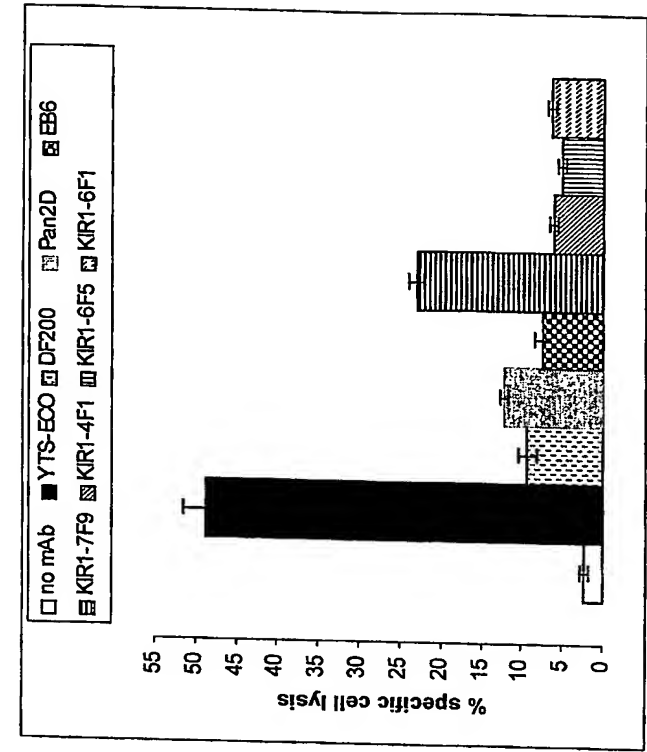
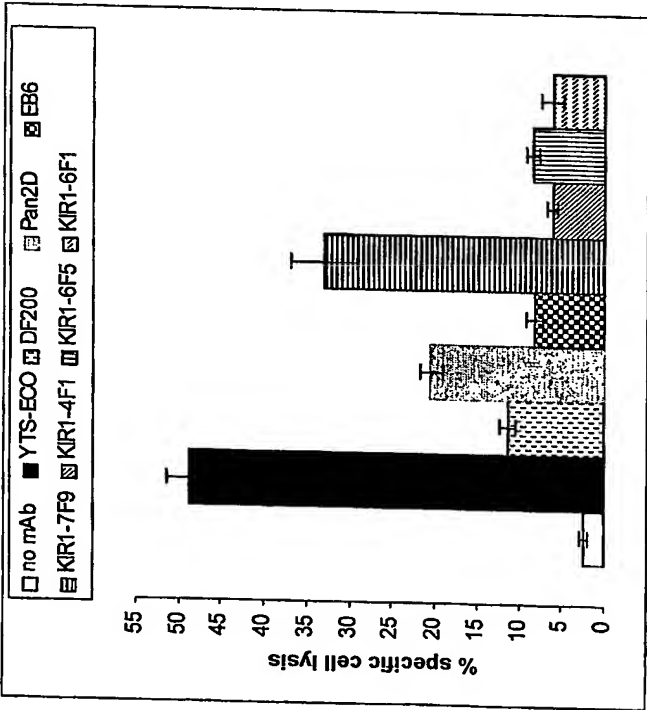


FIG 5A : mAb: 30µg/ml



E/T ratio= 1

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FIG 6

FIG 6B : mAb: 10µg/ml

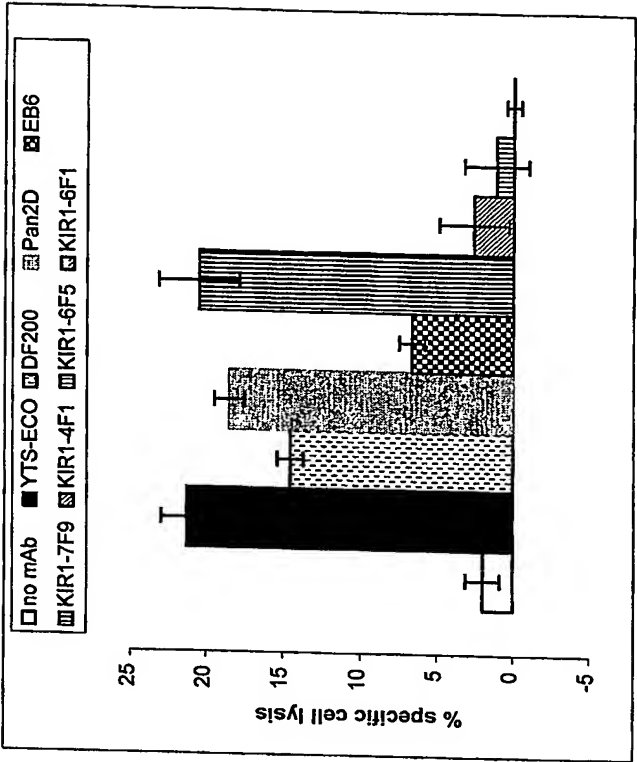
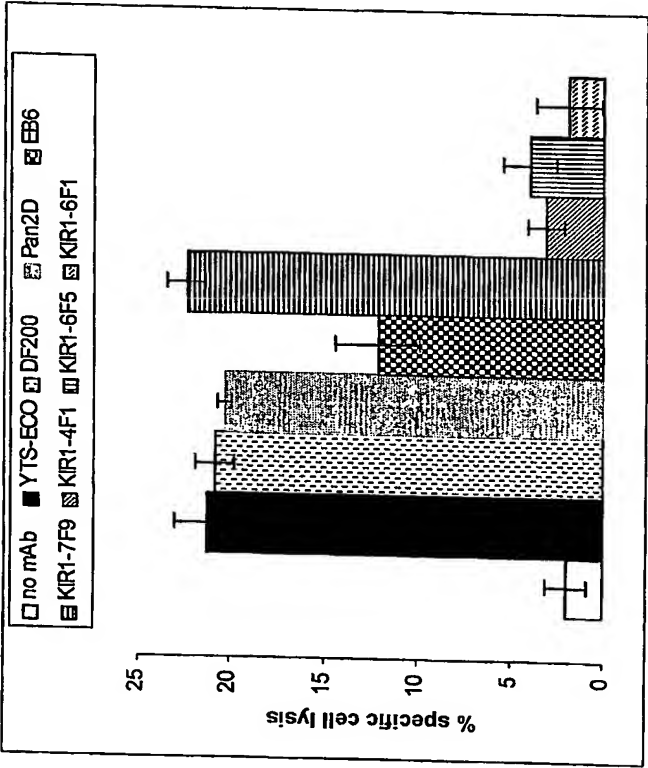


FIG 6A: mAb: 30µg/ml



E/T ratio= 2

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FIG 7

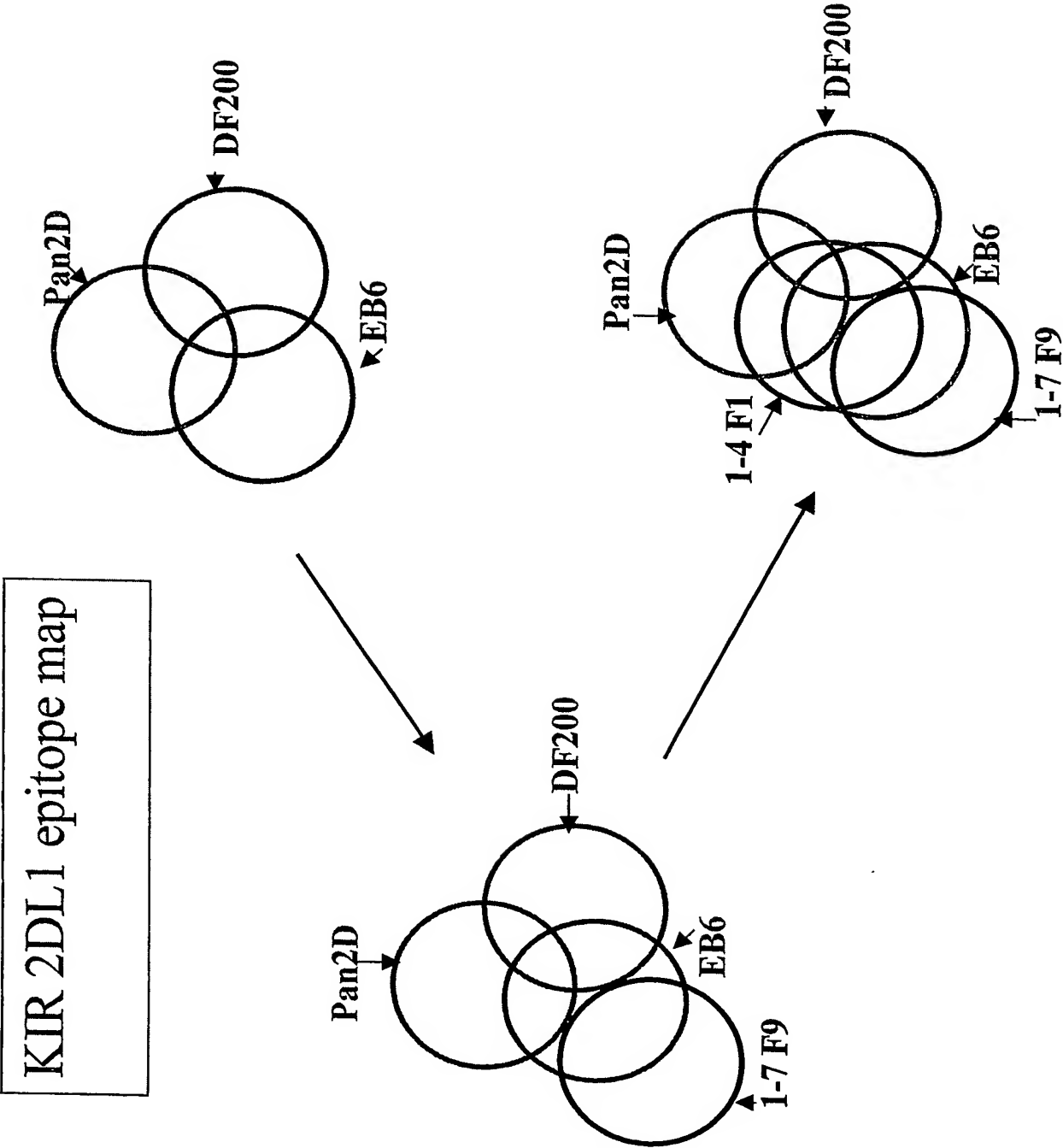
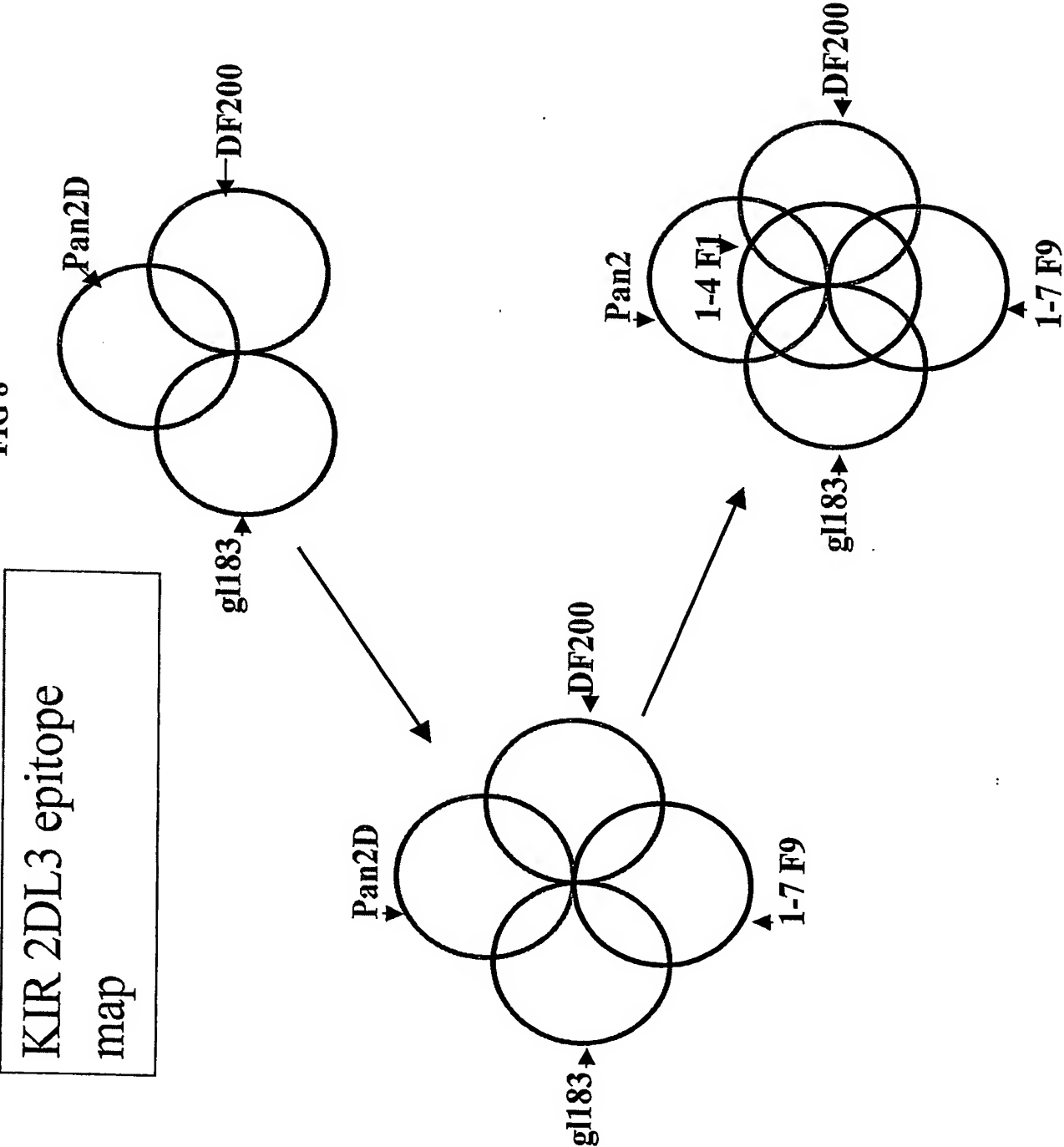


FIG 8





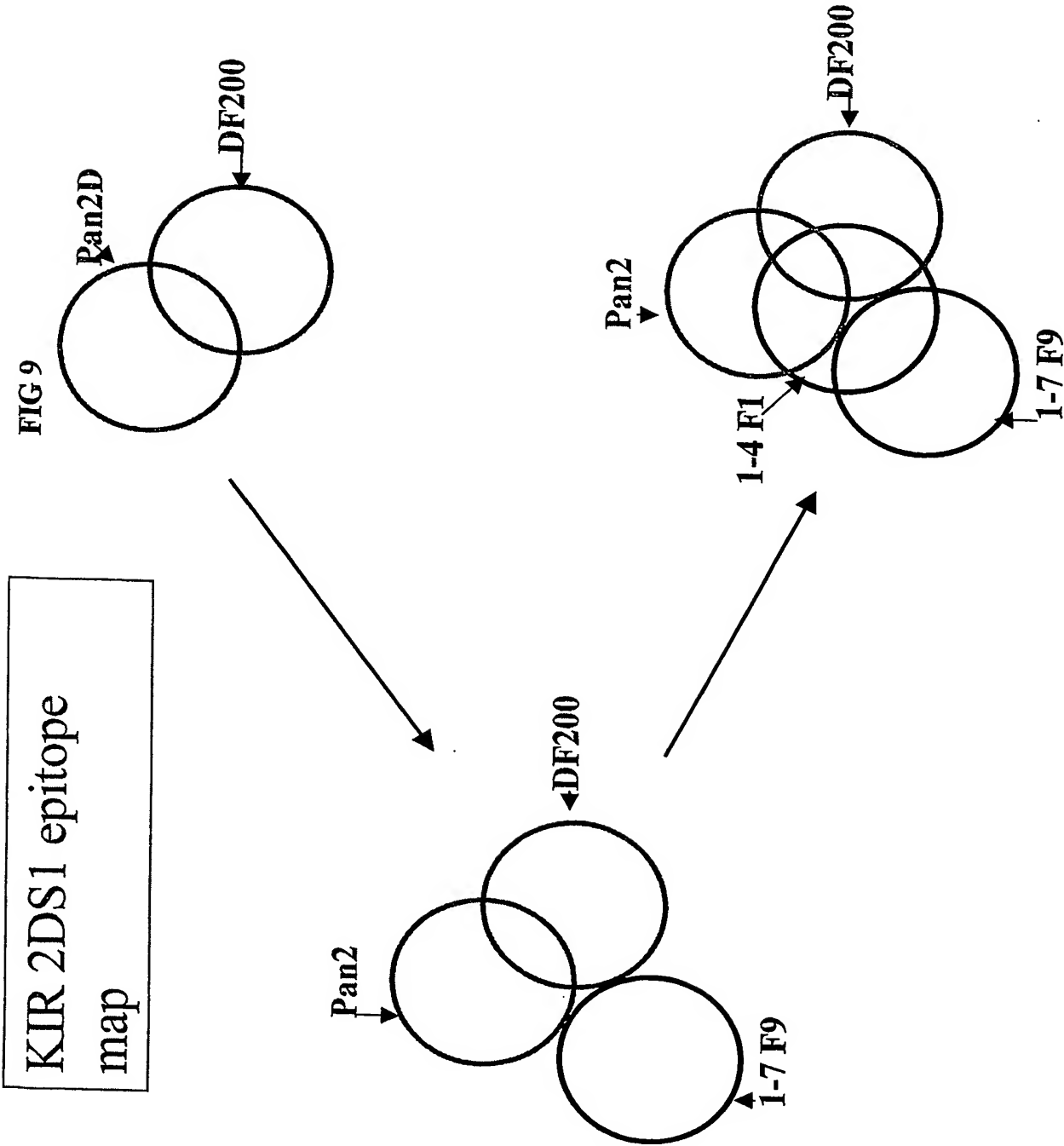
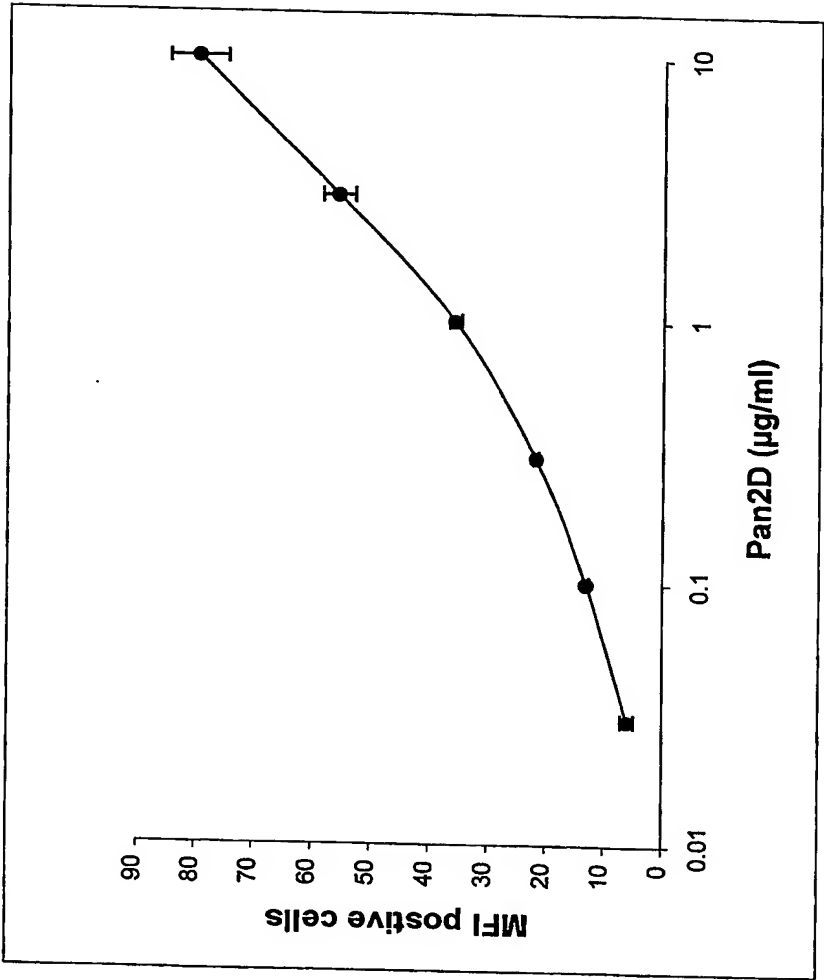


FIG 10



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FIG 11

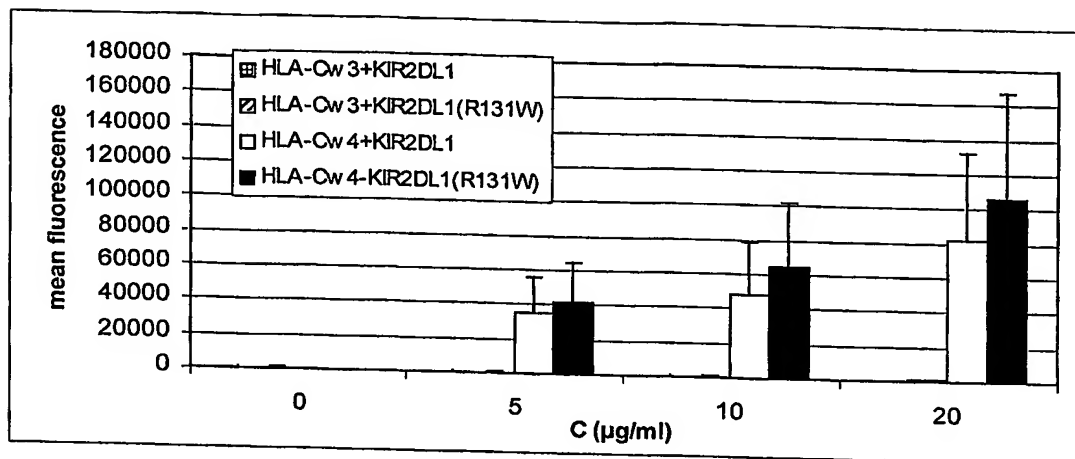
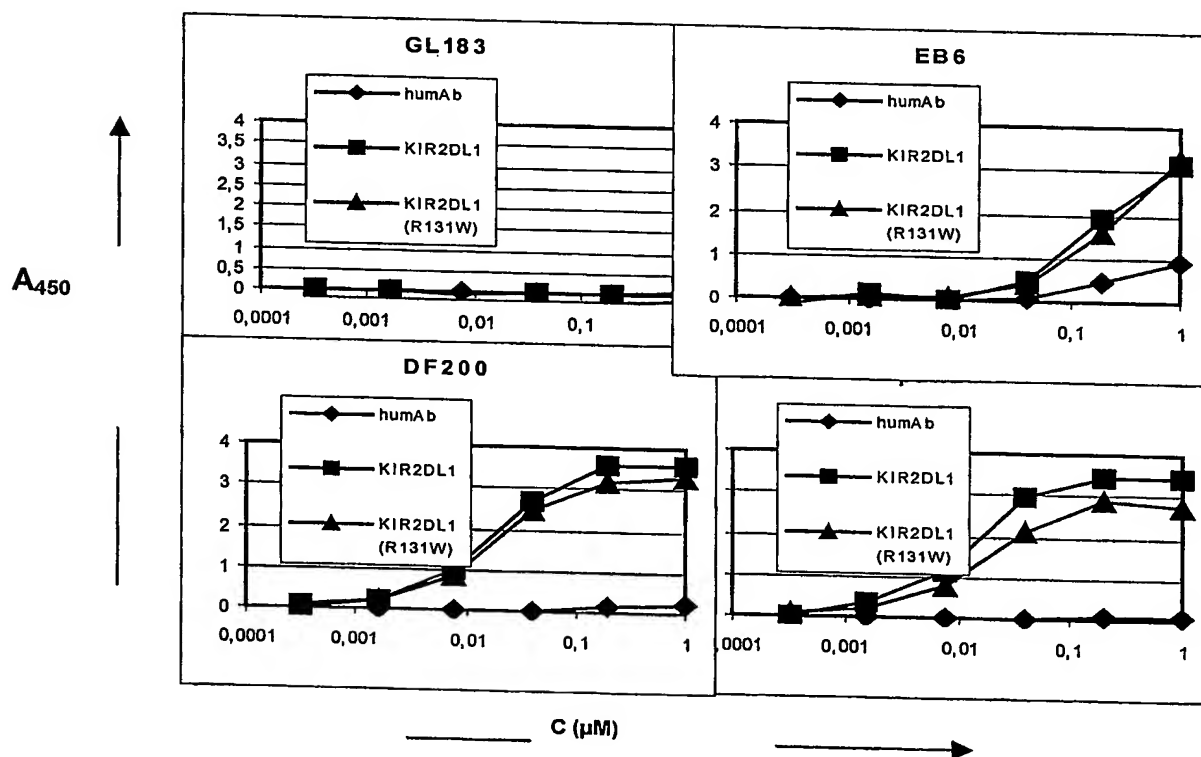
**FIG 11A** KIR2DL1(R131W)-hFc**FIG 11B**

FIG 12

**Anti-KIR light variable regions**

DF-200 light variable	(1)	M--ESQTLVFHSILLWLYGADGNIVMTQSPKSMMSVGERVTITCKASEN	50
PAN2D-Light-variable	(1)	MDFQVQIFSFLILISASIMSRGQIVETQSPASMSASVGERVTITCTASSS	
Consensus	(1)	Q F I I L A G N I V I T Q S P S M S S I G E R V T I T C A S	100
DF-200 light variable	(49)	VVT--VSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISS	100
PAN2D-Light-variable	(51)	VSSSTLYWYQQKPGSSPKLWYSTSNLASGVFARFSGSGGTSLTITISS	
Consensus	(51)	V S Y L W Y Q Q K P S P K L I Y S N S G V P R F S G S G S A T F S L T I S S	131
DF-200 light variable	(98)	QQAEDLADYHCGQGYSYPYTFGGGTKLEIKR	
PAN2D-Light-variable	(101)	MEAFDAATVCHQYERSPPTFGGGTKLEIKR	
Consensus	(101)	M A E D A Y H C Q H P T F G G G T K L E I K R	

Numbers above amino acid sequences indicate position respective to initiation of translation Met (+1) in the immature (non-secreted) immunoglobulin. Underlined are the CDR regions

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**CDR's from the anti-KIR light variable regions**

<b>CDR-L1 from clones PAN-2D and DF-200</b>		<b>CDR-L2 from clones PAN-2D and DF-200</b>	
Residue before: Normally Cys. Residues after: Trp. Typically Trp-Tyr-Leu.Length: 10-17 aa		Residues before: Generally Ile-Tyr Length: 7 aa Start: approximately 16 aa after the end of CDR-L1	
DF-200 light variable	(44) KASENVVT--YVS	DF-200 light variable	(70) GASNRYT
PAN2D-Light-variable	(46) TASSSVSSSYTY	PAN2D-Light-variable	(73) STSNLAS
Consensus	AS V S YL	Consensus	SN S
<b>CDR-L3 from clones PAN-2D and DF-200</b>			
Residues before: Cys			
Residues after: Phe-Gly-XXX-Gly			
Length: 7-11 aa			
Start: approximately 33 aa after the end of CDR-L2			
DF-200 light variable	(109) GQGYSYPYT		
PAN2D-Light-variable	(112) HQYERSPPT		
Consensus	Q H P T		

FIG 13

>DF-200\ VH\immature-PROT  
MAVLGLLFLCLVTFPSCVLS  
QVQLQSGPGLVQPSQSLTCTVSGFSFTPYGVHVVVRQSPGKGLEWLGVIWSGGNTDYNAAFISRLSINKDNSKSQVFFKMNSLQVND  
TAIYYCARNPRPGNYPYGMDYWGQGSTVTVSS

Anti-KIR heavy variable regions (immature Fabs)

Sequences including CDR regions in heavy variable regions

<b>CDR-H1 from clone DF-200</b> Residues before: Cys-XXX-XXX-XXX Residues after: Trp. Generally Trp-Val or Trp-Ile Length: 10-14 aa Start: Approximately 22-26 aa from the beginning of the secreted protein  GFSFTPYGVH	<b>CDR-H2 from clone DF-200</b> Residues before: Leu-Glu-Trp-Ile-Gly but other variations possible Residues after: Lys or Arg / Leu or Ile or Val or Phe or Thr or Ala / Thr or Ser or Ile or Ala Length: 16-20 aa Start: Approximately 15 aa after the end of CDR-H1  VIWSGGNTDYNAAFIS
<b>CDR-H3 from clones 4G1, 5D5 and 6C12</b> Residues before: Cys-XXX-XXX (Typically Cys-Ala-Arg) Residues after: Trp-Gly-XXX-Gly Length: 3-25 aa Start: Approximately 33 after the end of CDR-H2  NPRPGNYPYGMDY	

The secreted, mature VH starts at:  
Position 20: residue Q

The VH region ends with residue S and thereafter the constant region (not shown ) continues